



Review Article

Multi-Omics Machine Learning Models for Precision Cancer Prognostication

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Background: Cancer remains a leading cause of mortality worldwide, necessitating accurate prognostic tools to guide clinical decision-making and personalized treatment strategies. Traditional prognostic models based on clinicopathological features demonstrate limited predictive accuracy due to the inherent molecular heterogeneity of malignancies. This narrative review examines recent advances in multi-omics machine learning approaches for cancer prognosis prediction, synthesizing evidence from 2020–2026 on integration strategies, algorithmic methodologies, and clinical applications across major cancer types. Deep learning enables the analysis of high-dimensional datasets and the discovery of novel disease mechanisms and biomarkers, contributing to improved patient treatment and management. Multi-omics integration incorporating genomics, transcriptomics, epigenomics, proteomics, and metabolomics consistently outperforms single-omics approaches. DeepProg, a novel ensemble framework of deep-learning and machine-learning approaches, robustly predicts patient survival subtypes using multi-omics data and yields significantly better risk-stratification than other multi-omics integration methods. Graph neural networks, transformer-based architectures, and attention mechanisms have emerged as powerful tools for capturing complex inter-omics relationships. CATfusion achieves superior predictive performance over traditional and unimodal models, as demonstrated by enhanced C-index and survival area under the curve scores. These models demonstrate substantial improvements in survival prediction, recurrence risk stratification, and treatment response assessment across breast, lung, colorectal, liver, and hematological malignancies. Meta-learning, spatial multi-omics, and federated learning are pivotal directions for realizing the clinical translation of next-generation precision oncology. Addressing challenges in data harmonization, model interpretability, and prospective validation remains essential for clinical implementation.

Keywords: Multi-omics, machine learning, deep learning, cancer prognosis, precision oncology, data integration, survival prediction.

INTRODUCTION

Cancer represents one of the most significant global health challenges, accounting for millions of deaths annually and imposing substantial burdens on healthcare systems worldwide. Lung cancer remains the leading cause of cancer-related mortality worldwide, largely due to late-stage diagnosis, pronounced molecular heterogeneity, and variable therapeutic responses. (5) The clinical management of

cancer patients critically depends on accurate prognostic assessment to guide treatment decisions, optimize therapeutic strategies, and improve survival outcomes. Traditional prognostic models rely primarily on clinicopathological features including tumor stage, histological grade, and performance status. However, these conventional approaches demonstrate significant limitations in capturing the biological complexity underlying tumor behavior.

Combining omics data and demographic/clinical information can offer a more comprehensive view of cancer prognosis than using omics or clinical data alone and can also reveal the underlying disease mechanisms at the molecular level. (6) The emergence of precision oncology has fundamentally transformed cancer management by enabling molecularly-guided therapeutic strategies tailored to individual tumor characteristics. Recent advances in machine learning-driven multiomics technologies, including genomics, epigenomics, transcriptomics, proteomics, metabolomics, pathomics, and radiomics, have facilitated a deeper understanding of cancer by integrating molecular and imaging data. (7) Multi-omics approaches provide complementary information across multiple biological layers, capturing the hierarchical complexity of tumor biology from genomic alterations to functional protein expression and metabolic phenotypes. Advances in multi-omics profiling spanning genomics, transcriptomics, epigenomics, proteomics, and metabolomics have enabled finer subtype stratification and more comprehensive characterisation of tumour biology, thereby accelerating the discovery of diagnostic and prognostic biomarkers and actionable therapeutic targets. (8) The integration of these diverse data types presents substantial computational challenges due to high dimensionality, data heterogeneity, and the need to model complex non-linear interactions between molecular features. Machine learning and deep learning methodologies have emerged as powerful computational frameworks for addressing these challenges. Deep learning integrates high-dimensional data from fields such as genomics, epigenomics, transcriptomics, proteomics, radiomics, and single-cell omics, enhancing our understanding of cancer development and advancing personalized treatment approaches. (9) These approaches enable the extraction of clinically meaningful patterns from complex multi-dimensional datasets, facilitating improved risk stratification and outcome prediction. Machine learning and deep learning models support cancer phenotyping, including tumor detection, molecular subtyping, prognosis, and treatment response prediction across histopathology, radiology, and multi-omics data. (10) The convergence of multi-omics data generation with advanced computational methodologies represents a paradigm shift toward

data-driven precision oncology, promising more accurate and personalized cancer prognostication.

2. Multi-Omics Data in Cancer Research

2.1 Genomics

Genomic profiling constitutes the foundation of molecular cancer characterization, encompassing somatic mutations, copy number alterations, and structural variants. Genomic profiling has revealed recurrent mutations and subtype-specific aberrations, while transcriptomic analyses refine molecular classification and uncover alternative splicing and fusion events. (11) Somatic mutations in driver genes including TP53, KRAS, EGFR, and BRAF represent key determinants of tumor behavior and therapeutic vulnerability. Established genetic markers, such as IDH mutation and 1p/19q codeletion, are linked to glioma prognosis, and there is a critical need to identify novel targets associated with recurrence to overcome therapeutic challenges. (12) Copy number alterations affecting oncogenes and tumor suppressors contribute substantially to cancer progression. Tumor mutational burden has emerged as an important biomarker for immunotherapy response prediction, reflecting the neoantigen landscape and potential immunogenicity of tumors. Circulating tumor DNA assays now detect tumour-specific mutations, copy-number changes, and methylation patterns with higher sensitivity than PSA, enabling non-invasive early diagnosis, longitudinal monitoring of minimal residual disease, and real-time tracking of clonal evolution under therapeutic pressure. (13)

2.2 Transcriptomics

Gene expression profiling through RNA sequencing provides comprehensive insights into tumor biology and cellular state. Understanding cancer mechanisms, defining subtypes, predicting prognosis and assessing therapy efficacy are crucial aspects of cancer research. Gene-expression signatures derived from bulk gene expression data have played a significant role in these endeavors over the past decade. (14) The newer molecular platform, such as next-generation sequencing, including RNA-sequencing, single-cell sequencing, and microarray technology, has revolutionized the field of genomics, opened a new perspective in defining genetic and epigenetic

characteristics identifying molecules as possible therapeutic targets. (15) Transcriptomic signatures enable molecular subtype classification and provide prognostic information independent of clinical staging systems.

2.3 Epigenomics

Epigenetic modifications including DNA methylation and histone modifications represent reversible regulatory mechanisms with profound implications for cancer development and progression. Epigenetic profiling, basically at the level of DNA methylation and histone modifications, is starting to provide clinical value in the diagnosis, prognosis and prediction of response to drug therapies. (16) This review highlights the frequent occurrence of tumor suppressor gene hypermethylation and oncogene hypomethylation across various cancers. Additionally, changes in histone modifications, such as acetylation, methylation, and phosphorylation, can alter chromatin configuration and play a significant role in the emergence of oncogenic characteristics. (17) DNA methylation usually occurs in the very early stage of malignant tumors. Thus, DNA methylation analysis may provide some useful information about the early detection of lung cancer. (18) The MGMT promoter methylation status represents a clinically established epigenetic biomarker predicting response to alkylating chemotherapy in glioblastoma.

2.4 Proteomics

Proteomic profiling captures the functional molecular effectors executing cellular processes, providing information not directly inferable from genomic or transcriptomic data. Proteomics strategies appear as promising tools to comprehensively profile the final molecular effector of these cells. (19) Post-translational modifications including phosphorylation, ubiquitination, and glycosylation further expand the proteomic landscape influencing cancer phenotypes. Multi-omics clustering not only recapitulated established molecular subtypes but also revealed subtypes associated with chemotherapy sensitivity. Protein isoform level analysis identifies protein abundance of a short isoform of ATAD1 and RAF family proteins as biomarkers of chemosensitivity. (20)

2.5 Metabolomics

Metabolic reprogramming represents a hallmark of cancer, with altered metabolic signatures reflecting tumor phenotype and microenvironmental interactions. Metabolomics, leveraging mass spectrometry and nuclear magnetic resonance spectroscopy, offers a comprehensive and functional readout of tumor biochemistry. By enabling both targeted metabolite quantification and untargeted profiling, metabolomics captures the dynamic metabolic alterations associated with cancer. (21)

2.6 Single-Cell and Spatial Omics

Single-cell RNA sequencing profiles single-cell transcriptomes to reveal cell proportions and trajectories while spatial information is lacking. Spatially resolved transcriptomics redeems this lack with limited coverage or depth of transcripts. Hence, the integration of single-cell RNA sequencing and spatial data makes the best use of their strengths, having insights into exploring diverse tissue architectures and interactions in a complicated network. (22) Spatial transcriptomics in combination with single-cell RNA sequencing was used to decipher the spatially resolved cellular and molecular composition of colorectal cancer, mapping the intratumoral heterogeneity of consensus molecular subtypes and their microenvironment. (23) These emerging technologies enable unprecedented resolution in characterizing tumor microenvironment complexity and spatial organization.

3. Machine Learning Approaches for Cancer Prognostication

3.1 Traditional Machine Learning

Classical machine learning algorithms including logistic regression, support vector machines, random forests, and gradient boosting methods have established foundational roles in cancer prognosis prediction. Machine learning, with its ability to process high-dimensional data and identify complex patterns, offers a promising approach for cancer patients. Integrated models combining computational techniques with large multi-omics datasets have gained significant attention, enabling the identification of significant cancer biomarkers. (24)

DNA methylation outperforms other molecular data (mRNA expression and miRNA expression) in terms of accuracy and stability for discriminating between early stage and late stage groups. Furthermore, integration of multi-omics data by autoencoder can enhance the classification accuracy of cancer stage. (25) Random forests and gradient boosting methods demonstrate particular utility for feature selection and handling high-dimensional sparse data. The gradient boosting model predicted the most optimistic survival, while random forest showed a sharp decline after 15 months. The highest predictive accuracy (AUC: 0.947; accuracy: 56.8%) was observed in patients receiving both chemotherapy and radiation. (26)

3.2 Deep Learning Architectures

Deep learning has revolutionized cancer prognostication by enabling automatic feature extraction from raw high-dimensional data. By applying denoising Autoencoder to 15 cancers from The Cancer Genome Atlas, the method was shown to improve the C-index values over previous methods by 6.5% on average. (27) The proposed model combining Bi-directional Long Short-Term Memory and Convolutional Neural Network architectures, integrated with feature selection, achieved an accuracy of 98% on the METABRIC dataset and 96% on the TCGA dataset for breast cancer survival prediction. (28) A convolutional autoencoder prognostic model incorporating a channel attention mechanism (CA-CAE) utilizes multi-omics data to predict survival-associated cancer subtypes and identify prognostic genes, successfully identifying subtypes in 15 distinct cancer types and revealing significant survival differences among these subtypes. (29) Hybrid Deep Synergy, a novel hybrid deep learning model that integrates Convolutional Neural Networks, Long Short-Term Memory, and Transformer attention mechanisms, demonstrated superior performance achieving lower RMSE of 3.911 and higher coefficient of determination R^2 of 0.953. (30)

3.3 Transformer-Based Models and Foundation Models

Transformer architectures with attention mechanisms have emerged as powerful tools for multi-omics

integration and survival prediction. CATfusion, a deep learning framework that integrates multimodal histology-genomic data, employs self-supervised learning strategy with TabAE for feature extraction and utilizes cross-attention mechanisms to fuse diverse data types, including mRNA-seq, miRNA-seq, copy number variation, DNA methylation variation, mutation data, and histopathological images. (3) A multi-omics integrative methodology entailing integration of genomics, transcriptomics, proteomics, methylomics, and radiomics with hierarchical deep neural networks and transformer-based survival prediction models combines cross-modality transformer for capturing inter-omic relationships in an adaptive manner. (31) An outcome supervised deep learning model using a Vision Transformer network based on hematoxylin and eosin-stained specimens achieved an accuracy of 88.6% in the internal validation cohort and 81% in the external validation cohort for predicting immunotherapy efficacy in NSCLC patients. (32) The ongoing advancements in AI algorithms, particularly foundation models, generalist models and transformer-based deep learning, offer immense promise for the future of cancer research and care. (33)

4. Multi-Omics Data Integration Strategies

4.1 Early Integration

Early integration concatenates all omics datasets into a single matrix on which machine learning models can be applied. (34) This straightforward approach enables direct learning of cross-omics interactions but faces challenges with high dimensionality and modality imbalance. Early-intermediate fusion can stabilize high-dimensional inputs but is sensitive to modality imbalance. (35)

4.2 Intermediate Integration

Intermediate integration simultaneously transforms the original datasets into common and omics-specific representations. (34) This strategy enables learning of shared latent representations while preserving modality-specific information. The Intermediate Fusion method, which combines deep features from a ResNet-18 with radiomic features at an intermediate layer, achieved the highest overall predictive

performance for both EGFR (Accuracy: 0.986) and KRAS (Accuracy: 0.97) mutations, suggesting that integrating learned and hand-crafted features within the network itself is the most effective strategy. (36)

4.3 Late Integration

Late integration analyses each omics separately and combines their final predictions. (34) Late integration modeling approaches analyze each data modality separately to obtain modality-specific predictions. These predictions are then aggregated into a meta-model by training a machine learning model, or by computing the weighted mean of modality-specific predictions. (37) Experimental findings reveal that Late-Fusion produces better performance, achieving 96.96% Accuracy, 96.86% Precision, 96.89% Recall, and 96.87% F1-score in comparison to Early-Fusion strategies. Results suggest that Late-Fusion not only enhances predictive performance but also maintains the biological interpretability crucial for integration of multi-omics in cancer research. (38) Across all modality combinations, late fusion models consistently outperformed early fusion approaches and late and intermediate benchmark methods, with the combination of omics and clinical data yielding the highest test-set concordance indices. (39)

4.4 Network-Based Integration and Graph Neural Networks

MMGCN utilizes the similarity network fusion algorithm to merge patient similarity networks, individually constructed using gene expression, copy number alteration, and clinical data, into a fused patient similarity network for integrating multi-modal information. (40) Geometric graph neural networks incorporate geometric features into deep learning for enhanced predictive power and interpretability, utilizing a state-of-the-art graph neural network with sparse connections between the hidden layers based on known biology of the protein-protein interaction network and pathway information. (41) MoJKNet incorporates a jumping knowledge network to adaptively aggregate node representations across multiple propagation depths, thereby alleviating over-smoothing and enhancing feature extraction within each omics modality, consistently outperforming state-of-the-art methods including MOGCAN, MOGONET, and MoGCN. (42)

4.5 Multi-View Learning and Federated Approaches

A multi-omics data fusion algorithm based on a multi-view graph neural network consists of a graph convolutional network module for learning features from different omics data and an attention module for integrating multi-omics data, performing well in cancer classification prediction. (43) Cancer bioinformatics has evolved from single-omics analyses to integrated multi-omics approaches. Key innovations like the CancerSD model address incomplete data challenges, while single-cell and spatial omics technologies reveal intra-tumoral dynamics and microenvironment interactions. (44)

5. Applications of Multi-Omics Machine Learning Models in Precision Cancer Prognostication

5.1 Breast Cancer

Breast cancer represents the most extensively studied malignancy for multi-omics prognostication. The deep learning model for multi-omics data significantly outperformed single-omics models in subtype prediction, achieving a 98.0% accuracy in cross-validation, 97.0% in the validation set, and 91.0% in an external test set for triple-negative breast cancer classification and prognosis prediction. (45) The survival prediction framework was highly effective in categorizing patients into risk subtypes with an accuracy of 94%. Compared to single-omics and early integration approaches, drug response prediction models performed significantly better and were able to predict IC50 values with a mean square error of 1.154 and an overall regression value of 0.92. (46) An immune-related lncRNA signature scoring system comprising nine key lncRNAs, validated across 17 independent cohorts, demonstrated that high-risk patients had significantly shorter overall survival, with predictive performance surpassing 95 published models. (47) Graph-based multi-omics fusion using similarity network fusion produced a stable two-cluster partition with NMI of 0.495 versus PAM50, exceeding RNA-only (0.428) and early concatenation (0.175), achieving an out-of-fold C-index of 0.681. (48)

5.2 Lung Cancer

Novel actuarial deep learning neural network architectures integrating multi-omics information including PET radiomics, cytokines and miRNAs achieved c-indexes of 0.705 for radiation pneumonitis and 0.740 for local control prediction in stage III non-small-cell lung cancer, outperforming traditional NTCP/TCP models. (49) The Multi-Omics Lung Cancer Graph Network (MOLUNGN) based on Graph Attention Networks achieved accuracy of 0.84 and F1_macro of 0.82 on lung adenocarcinoma, and accuracy of 0.86 and F1_macro of 0.84 on lung squamous cell carcinoma for precise cancer staging classification. (50) A loosely supervised deep learning model utilizing convolutional neural network and transformer backbone to obtain features at the local nodule level and global contextual level performed better than radiomics- and clinical-only baselines with significantly improved concordance index, AUC, and calibration. (51)

5.3 Colorectal Cancer

Similarity network fusion exhibited exceptional performance in integrating multi-omics data, effectively distinguishing colorectal cancer patients into five subgroups with the highest classification accuracy and significant survival differences and molecular distinctions among subtypes. (52) Machine learning-based survival prediction models incorporating activated cancer-associated fibroblasts demonstrated superior prognostic accuracy for overall survival and disease-free survival compared to models excluding fibroblasts, with fibroblasts associated with advanced T stage, lymphovascular invasion, perineural invasion, and decreased CD8+ T cell infiltration. (53) CRCDB contains multi-omics data of 785 early-onset colorectal cancer, 4898 late-onset colorectal cancers, and 1110 normal control samples, revealing that genes associated with metabolic process were less expressed in early-onset colorectal cancer patients. (54)

5.4 Liver Cancer

DeepProg is highly predictive, exemplified by two liver cancer datasets achieving C-index 0.73-0.80 and five breast cancer datasets achieving C-index 0.68-0.73. (2) Integration of single-cell, bulk, and spatial transcriptome analyses classified three fibroblast subpopulations in hepatocellular carcinoma: HLA-

DRB1+ CAF, MMP11+ CAF, and VEGFA+ CAF, primarily located in normal tissue, tumor boundaries, and tumor interiors, respectively. VEGFA+ CAFs were significantly associated with patient survival and promoted intra-tumoral angiogenesis through cellular communication with capillary endothelial cells. (55) Single-cell and spatial transcriptomic analyses revealed co-localization relationships between hypoxia tumor cells, PLVAP+ endothelial cells, and VEGFA+ cancer-associated fibroblasts, suggesting a key role for hypoxia tumor cells in tumor angiogenesis in hepatocellular carcinoma. (56)

5.5 Prostate Cancer

Multi-omics prognostic signatures integrating mutation, expression, methylation, and immune features outperform traditional staging for predicting biochemical recurrence, metastasis, and treatment resistance in prostate cancer. (13)

5.6 Hematological Malignancies

From 2847 records, 89 studies met inclusion criteria for machine learning applications to multi-omics for molecular characterization of hematological malignancies, focusing on acute myeloid leukemia (34 studies), acute lymphoblastic leukemia (23 studies), and multiple myeloma (18 studies). The median diagnostic area under the curve was 0.87; deep learning reached 0.91 but offered the least explainability. (57) AI models demonstrate robust capabilities across diagnostic, prognostic, and therapeutic applications in multiple myeloma and lymphomas. Single-center studies report outstanding metrics, including AUCs up to 0.99 for myeloma lesion classification, while multicenter validation yields more conservative yet robust metrics. (58) Combining single-cell RNA sequencing with machine-learning methods for multiple myeloma identified prognostic gene signatures that, combined with international staging system scores, resulted in superior prediction of overall survival with a hazard ratio of 13.5 compared to 2.5 for ISS alone. (59)

CHALLENGES AND LIMITATIONS

6.1 High Dimensionality and Small Sample Size

It is challenging to effectively integrate multi-omics data due to the large number of redundant variables but relatively small sample size. (27) The curse of dimensionality poses significant challenges for model training and generalization. Longitudinal survival studies involving high-dimensional biomarker data are frequently challenged by pervasive missingness and limited sample sizes, which can compromise model stability and interpretability. (60)

6.2 Missing Omics Data and Batch Effects

One of the main challenges in integrating multi-omics data is handling missing data, since not all biomolecules are consistently measured across all samples. Current computational models based on multi-omics data for cancer subtyping often struggle with the challenge of weakly paired omics data. (61) We explore fundamental multi-omics challenges including batch effects, high dimensionality, and structural heterogeneity. (62) The algorithms blindly, without any assumptions or a-priori knowledge, removed batch effects and separated demographic variations from the data. (63)

6.3 Model Overfitting and Generalizability

A striking proportion of AI-identified biomarkers fail to advance beyond computational discovery due to poor reproducibility, lack of external validation, or inability to demonstrate added predictive value over established clinical markers. Many models are trained on small, unrepresentative datasets, leading to overfitting and limited generalizability. (64) The most critical challenge is the "validation gap"—many models show excellent single-institution performance but fail external validation, limiting clinical translation. (65)

6.4 Interpretability and Clinical Trust

The clinical adoption of most AI systems is still limited by the black box issue, that is, prediction without clear explanation, which limits the confidence and accountability of clinicians as well as their ability to communicate with patients. (66) External validation occurred in only 31 studies, and explainability in only 19 studies. Gaps in validation, interpretability, and standardization remain significant barriers. (57)

6.5 Clinical Validation and Regulatory Barriers

Despite advances, translation into routine clinical practice remains limited due to dataset bias, limited generalizability, the lack of standardized data protocols, insufficient interpretability and regulatory barriers. (67) There are currently no prognostic or predictive AI-based biomarkers supported by level IA or IB evidence. Several barriers for the adoption of AI in clinical workflows, such as data availability, explainability, and regulatory considerations, still persist. (33)

7. Clinical Translation and Future Perspectives

7.1 Explainable AI

Local interpretable model-agnostic explanation and Shapley additive explanations (LIME and SHAP) are model-agnostic methods that offer local and global feature attribution and help clinicians to understand the main influential factors behind model predictions. Gradient-weighted Class Activation Mapping (Grad-CAM), Integrated Gradients and DeepLift bring explainability to image- and genomics-based processes. (66) For computational interpretability, convolutional neural networks and multi-head attention mechanisms with SHAP analysis were employed. Compared to clinical-only models, multi-omics integration increased performance by 12%. (68)

7.2 Digital Pathology Integration

Using a deep-learning-based workflow, models were developed to predict clinicopathological features, multi-omics features and prognosis of patients with HR+/HER2– breast cancer using pathological whole-slide images, contributing to efficient patient stratification for personalized management. (69) Dual-stream multi-dependency graph neural networks enable precise cancer patient survival analysis from histopathology images, offering interpretable prediction insights based on morphological depiction of high-attention patches. (70)

7.3 Spatial Multi-Omics

AI-based spatial immunometabolism will be a cornerstone in precision oncology, with the potential

to improve patient stratification, therapeutic approaches, and clinical translation through multimodal foundation models, federated learning, and spatially resolved target discovery. (71) Pan-cancer analysis of stromal cells using single-cell RNA sequencing from 258 patients across 16 cancer types and spatial transcriptomics from 16 patients identified distinct features of 39 stromal subsets, including various functional modules, spatial locations, and clinical and therapeutic relevance. (72)

7.4 Foundation Models and Federated Learning

This article systematically reviews how artificial intelligence reshapes the multi-omics landscape, highlighting Graph Neural Networks for topological feature extraction and Transformers for constructing biological foundation models. (4) Artificial intelligence and machine learning are increasingly indispensable for fusing heterogeneous, high-dimensional data into deployable composite predictors and mechanistically grounded signatures. Future directions include single-cell and spatial multi-omics integration, federated learning, and generative modeling to accelerate robust, generalizable precision immunotherapy. (73) Emerging directions such as multimodal foundation models, federated learning, AI stewardship, and patient-specific digital twins outline a roadmap for integrating trustworthy AI into precision oncology. (10)

CONCLUSION

Multi-omics machine learning models represent a transformative paradigm for precision cancer prognostication, enabling comprehensive molecular characterization and accurate outcome prediction across diverse malignancy types. Accurate prognosis for cancer patients can provide critical information for optimizing treatment plans and improving life quality. (6) The integration of genomics, transcriptomics, epigenomics, proteomics, and metabolomics through sophisticated computational frameworks including deep neural networks, graph neural networks, and transformer architectures consistently demonstrates superior performance compared to single-omics or clinical-only approaches. Translating multi-layer molecular signals into clinically robust decision support remains challenging because of the high dimensionality and heterogeneity of omics data,

cross-cohort and cross-platform variability, and the fragmentation inherent to single-modality analyses. (8) Significant barriers to clinical translation persist, including limited external validation, model interpretability concerns, and the need for prospective clinical trials. Multidisciplinary collaboration, rigorous prospective validation and robust ethical governance will be essential to realize the full potential of AI in advancing precision oncology and improving global cancer outcomes. (67) The application of AI in pathology is poised to not only enhance the accuracy and efficiency of cancer diagnosis and prognosis but also facilitate the development of personalised treatment strategies. The continued evolution and adoption of AI in pathology and oncology are anticipated to reshape the landscape of cancer care, heralding a new era of precision medicine and improved patient outcomes. (33) Future advances in spatial multi-omics, foundation models, federated learning, and explainable AI promise to address current limitations and accelerate the clinical implementation of multi-omics machine learning models for truly personalized cancer management.

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